

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model  
Run on: March 27, 2006, 17:41:56 ; Search time 1143.19 Seconds  
(without alignments)  
12714.981 Million cell updates/sec

Title: US-10-623-272-56  
Perfect score: 2181  
Sequence: 1 cggcttaccatcacagca.....aaggctaccatgcaaggtga 2181

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues  
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : N Geneseq 21.\*
- 1: Geneseqn1980s.\*
  - 2: Geneseqn1990s.\*
  - 3: Geneseqn2000s.\*
  - 4: Geneseqn2001as.\*
  - 5: Geneseqn2001bs.\*
  - 6: Geneseqn2002as.\*
  - 7: Geneseqn2002bs.\*
  - 8: Geneseqn2003as.\*
  - 9: Geneseqn2003bs.\*
  - 10: Geneseqn2003cs.\*
  - 11: Geneseqn2003ds.\*
  - 12: Geneseqn2004as.\*
  - 13: Geneseqn2004bs.\*
  - 14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2181	100.0	2181	3	AAD00749 Human act
2	2169	99.4	4386	4	Aaf54895 Human act
3	2169	99.4	4462	5	ABA83022 Human tra
4	2169	99.4	4663	4	Aa158447 Human pol
5	2169	99.4	4663	5	ADQ98658 DNA encod
6	2169	99.4	4663	9	ADB48418 Novel hum
7	2169	99.4	4713	9	ADA07950 Human act
8	2169	99.4	4713	14	ADX06276 Cyclin-de
9	2165.8	99.3	4193	3	AAD00750 Human act
10	2140	98.1	4874	2	AAV49807 Human ADN
11	2140	98.1	4874	3	AAV49807 Human act
12	2128.6	97.6	4554	4	AA160233 Human pol
13	1961	89.9	4632	4	Aaf54902 Human act
14	1715.6	78.7	2487	3	AAD00748 Mouse act
15	1697.8	77.8	2421	2	AAV49808 Mouse ADN
16	1697.8	77.8	2421	3	AAD00747 Mouse act
17	1553	71.2	1766	4	Aa119537 Probe #94
18	1553	71.2	1766	4	ABA64554 Human foe
19	1553	71.2	1766	4	Aa144727 Probe #13

C 20	1553	71.2	1766	4	ABA46681	AbA46681 Human bre
C 21	1553	71.2	1766	4	AAX38731	Aak38731 Human bon
C 22	1553	71.2	1766	4	ABS38306	Abs38306 Human liv
C 23	1553	71.2	1766	5	AA105258	Aa105258 Probe #52
C 24	1553	71.2	1766	6	ABS12802	Abs12802 Human gen
C 25	1103.4	50.6	2420	4	AAX94337	Aak94337 Human ful
C 26	1103.4	50.6	2420	12	ADL30998	Adl30998 Full leng
C 27	791.4	36.3	852	4	AAK91980	Aak91980 Human CDN
C 28	791.4	36.3	852	4	AAK93971	Aak93971 Human CDN
C 29	791.4	36.3	852	12	ADL30398	Adl30398 5' end of
C 30	791.4	36.3	852	12	ADL28407	Adl28407 5' end of
C 31	720.8	33.0	938	2	AAX39926	Aax39926 Gastric c
C 32	607.4	27.8	772	4	AAK93336	Aak93336 Human CDN
C 33	607.4	27.8	772	12	ADL29763	Adl29763 5' end of
C 34	606	27.8	607	3	AAK79209	Aak79209 Human lun
C 35	606	27.8	607	10	ADD6559	Add6559 Human lun
C 36	606	27.8	607	10	ADD6559	Add6559 Human lun
C 37	606	27.8	607	10	ADD6559	Add6559 Human lun
C 38	471	21.6	471	4	ABA51894	AbA51894 Human foe
C 39	471	21.6	471	4	AAI10258	Aai10258 Probe #19
C 40	471	21.6	471	4	AAI31505	Aai31505 Probe #19
C 41	471	21.6	471	4	AAK25631	Aak25631 Human bon
C 42	471	21.6	471	4	ABS25208	Abs25208 Human liv
C 43	471	21.6	471	5	AAI00195	Aai00195 Probe #18
C 44	471	21.6	471	6	ABS00200	Abs00200 Human gen
C 45	395	18.1	396	10	ADD67006	Add67006 Human lun

ALIGNMENTS

RESULT 1

AAD00749  
ID AAD00749 standard; CDNA; 2181 BP.

AC AAD00749;

DT 08-SEP-2000 (first entry)

XX Human Activity Dependent Neurotrophic Factor (ADNF) III H3 CDNA.

DE Activity Dependent Neurotrophic Factor III; ADNF; human; ADNP;  
KW Activity Dependent Neuroprotective Protein; chromosome 20q13.2; ADNFLE;  
KW Autosomal dominant nocturnal frontal-lobe epilepsy; neuronal cell death;  
KW Neurological deficiency; treatment; HIV; Human Immunodeficiency Virus;  
KW Alzheimer's disease; beta-amyloid peptide; Huntington's disease;  
KW epilepsy; AIDS dementia complex; neuropathic pain syndrome; ALS;  
KW anyotrophic lateral sclerosis; Parkinson's disease; Leber's disease;  
KW mitochondrial abnormality; Wernicke's encephalopathy; homocysteinuria;  
KW hyperprolinemia; sulphite oxide disease; Tourette's syndrome; nootropic;  
KW Down's syndrome; drug addiction; developmental retardation; antileptic;  
KW learning impairment; anticonvulsant; neuroprotective; anti-HIV; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..2181

FT FT /\*tag= a

FT FT /product= "Human ADNF III H3 protein"

FT FT /transl\_except= (pos:997..999, aa:Tyr)

XX XX /note= "Activity Dependent Neurotrophic Factor III"

XX WO200027875-A2.

XX 18-MAY-2000.

XX 04-NOV-1999; 99WO-US026213.

XX 06-NOV-1998; 98US-00187330.

XX (USAS ) GOVERNMENT US REPRESENT AS.

XX (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

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OM nucleic - nucleic search, using sw model

Run on: March 27, 2006, 18:29:37 ; Search time 922.152 Seconds  
(without alignment)  
9427.972 Million cell updates/sec

Title: US-10-623-272-56

Perfect score: 2181

Sequence: 1 cggctttacatcacagca.....aagctaccatgcaggtga 2181

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9258654 seqs, 1993127192 residues

Total number of hits satisfying chosen parameters: 18517308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:\*

- 1: /SIDSS/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 2: /SIDSS/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /SIDSS/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 4: /SIDSS/ptodata/2/pubpna/ECT\_NEW\_PUB.seq.\*
- 5: /SIDSS/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 6: /SIDSS/ptodata/2/pubpna/US09\_NEW\_PUB.seq.1\*
- 7: /SIDSS/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 8: /SIDSS/ptodata/2/pubpna/US10\_NEW\_PUB.seq.1\*
- 9: /SIDSS/ptodata/2/pubpna/US10\_NEW\_PUB.seq.2\*
- 10: /SIDSS/ptodata/2/pubpna/US10\_NEW\_PUB.seq.3\*
- 11: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 12: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq.2\*
- 13: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq.3\*
- 14: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq.4\*
- 15: /SIDSS/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42.8	2.0	1452	9	US-10-932-182A-78450
2	42.8	2.0	1452	9	US-10-932-182A-78450
3	41.8	1.9	995	10	US-10-301-480-531242
4	41.8	1.9	995	10	US-10-301-480-1144651
5	41.8	1.9	2412	9	US-10-932-182A-6042
6	41.8	1.9	2412	9	US-10-932-182A-6042
7	41	1.9	1020	9	US-10-932-182A-77008
8	41	1.9	1020	9	US-10-932-182A-77008
9	39.8	1.8	1419	14	US-11-055-822-1095
10	39.6	1.8	576	6	US-09-925-065A-484403
11	39.4	1.8	609	6	US-09-925-065A-232485
12	39.4	1.8	627	10	US-10-301-480-315790
13	39.4	1.8	627	10	US-10-301-480-929199
14	39.2	1.8	1758	9	US-10-932-182A-76904
15	39.2	1.8	1758	9	US-10-932-182A-76904
16	39.2	1.8	2787	9	US-10-932-182A-80470
17	39.2	1.8	2787	9	US-10-932-182A-80470
18	38.8	1.8	564	6	US-09-925-065A-298577

19	38.8	1.8	564	6	US-09-925-065A-298578	Sequence 298578,
20	38.8	1.8	574	10	US-10-301-480-375216	Sequence 375216,
21	38.8	1.8	574	10	US-10-301-480-375217	Sequence 375217,
22	38.8	1.8	574	10	US-10-301-480-988625	Sequence 988625,
23	38.8	1.8	574	10	US-10-301-480-988625	Sequence 988625,
24	38.8	1.8	582	9	US-10-301-480-79721	Sequence 79721, A
25	38.8	1.8	582	10	US-10-301-480-693130	Sequence 693130,
26	38.8	1.8	642	9	US-10-301-480-62473	Sequence 62473, A
27	38.8	1.8	642	10	US-10-301-480-675882	Sequence 675882,
28	38.4	1.8	1121	11	US-11-096-568A-6242	Sequence 6242, Ap
29	38	1.7	599	6	US-09-925-065A-645144	Sequence 645144,
30	38	1.7	2184	9	US-10-932-182A-77555	Sequence 77555, A
31	38	1.7	2184	9	US-10-932-182A-77555	Sequence 77555, A
32	37.6	1.7	537	9	US-10-301-480-19979	Sequence 19979, A
33	37.6	1.7	537	10	US-10-301-480-633388	Sequence 633388,
34	37.6	1.7	582	9	US-10-301-480-79719	Sequence 79719, A
35	37.6	1.7	582	9	US-10-301-480-79720	Sequence 79720, A
36	37.6	1.7	582	10	US-10-301-480-693128	Sequence 693128,
37	37.6	1.7	582	10	US-10-301-480-693129	Sequence 693129,
38	37.6	1.7	680	6	US-09-925-065A-285811	Sequence 285811,
39	37.6	1.7	685	10	US-10-301-480-362805	Sequence 362805,
40	37.6	1.7	685	10	US-10-301-480-976214	Sequence 976214,
41	37.6	1.7	161874	14	US-11-121-086-75	Sequence 75, Appl
42	37.4	1.7	568	10	US-10-301-480-236580	Sequence 236580,
43	37.4	1.7	568	10	US-10-301-480-849989	Sequence 849989,
44	37.4	1.7	570	6	US-09-925-065A-141735	Sequence 141735,
45	37.4	1.7	644	6	US-09-925-065A-595340	Sequence 595340,

ALIGNMENTS

RESULT 1

US-10-932-182A-78450  
; Sequence 78450, Application US/10932182A  
; Publication No. US20060046253A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: 030685-043  
; CURRENT APPLICATION NUMBER: US/10/932,182A  
; CURRENT FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 78450  
; LENGTH: 1452  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-10-932-182A-78450

Query Match 2.0% Score 42.8; DB 9; Length 1452;

Best Local Similarity 46.6%; Pred. No. 0.6; Indels 0; Gaps 0;  
Matches 137; Conservative 0; Mismatches 157;

Qy	1732	GACAGTCTCCTCAGACAGTCTTGAATAATTTGGAAGAAGATCCCAATGAAGTGGTAGCCCT	1791
Db	697	GACAGCATGAGATATGTCAGAGAGAGAGAGAGAAATAATGTTATCTTAATGAC	755
Qy	1792	TTTGACCCCTGTTTTGAAGTTGAACCTTAAATCTTCAACGATACCCAGAGGAACATGTA	1851
Db	757	CTATTAAGGACCTTTGACTTCGATTAACCAATGACGTTGAATGATTCGAGGAGAACTT	816
Qy	1852	CTGAGGATTAATCTTGAGGATGCTTCAGATCTTGAGGAGAGCTAGACCAAAAGAGAT	1911
Db	817	CTGACAGCAACCTGTAAGGAGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGATTAAC	876
Qy	1912	GGTTCAAAATACGAAATCTTTCATTTGACTTGAGGAACCAACCAATTAATGCAATGCA	1971
Db	877	GCTCCCGATACGAGATGTTAATAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	936

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OM nucleic - nucleic search, using sw model

Run on: March 27, 2006, 18:11:13 ; Search time 1513.77 Seconds  
(without alignments)

11914.334 Million cell updates/sec

Title: US-10-623-272-56

Perfect score: 2181

Sequence: 1 cggctttaccatcacagca.....aaggctaccatgcaaggtga 2181

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA Main:

- 1: /cgn2\_6/ptodata/1/pubna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubna/US08\_PUBCOMB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubna/US09A\_PUBCOMB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubna/US09B\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubna/US10A\_PUBCOMB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubna/US10B\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubna/US10C\_PUBCOMB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubna/US10D\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubna/US10E\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2181	100.0	2181	7	US-10-623-272-56
2	2169	99.4	4386	3	US-09-364-609-7
3	2169	99.4	4462	3	US-10-221-625-156
4	2169	99.4	4663	5	US-10-037-270-328
5	2169	99.4	4663	6	US-10-117-722-328
6	2169	99.4	4663	9	US-10-122-851-328
7	2169	99.4	4713	6	US-10-164-432-1
8	2165.8	99.3	4193	7	US-10-623-272-58
9	2140	98.1	4874	7	US-10-623-272-2
10	1715.6	78.7	2487	7	US-10-623-272-54
11	1697.8	77.8	2421	7	US-10-623-272-4
12	1553	71.2	1766	3	US-09-864-761-30357
13	606	27.8	607	3	US-09-738-973-251
14	606	27.8	607	3	US-09-854-133-251
15	606	27.8	607	5	US-10-144-649A-251
16	471	21.6	471	3	US-09-864-761-13787
17	395	18.1	396	3	US-09-854-133-698
18	395	18.1	396	5	US-10-144-649A-698
19	383.6	17.6	837	7	US-10-623-272-29
20	383.6	17.6	850	7	US-10-623-272-30
21	373.4	17.1	564	5	US-10-060-036-856
22	348.8	16.0	352	3	US-09-777-564-104
23	348.8	16.0	352	5	US-10-015-219-104

Sequence 1874, App  
Sequence 7, Appl  
Sequence 1152, App  
Sequence 9412, App  
Sequence 252, App  
Sequence 680, App  
Sequence 944, App  
Sequence 6326, App  
Sequence 23112, A  
Sequence 4311, App  
Sequence 4312, App  
Sequence 14893, A  
Sequence 90597, A  
Sequence 2523, App  
Sequence 2222, App  
Sequence 29690, A  
Sequence 600, App  
Sequence 346, App  
Sequence 346, App  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 20772, A

24 312 14.3 399 3 US-09-960-352-1874  
25 215.2 9.9 267 5 US-10-140-463-7  
26 125.8 5.8 627 3 US-09-969-034-1152  
27 99.2 4.5 502 6 US-10-029-386-9412  
28 99.2 4.5 821 3 US-09-764-864-252  
29 99.2 4.5 2127 3 US-09-764-864-680  
30 99.2 4.5 2127 3 US-09-764-864-680  
31 99.2 4.5 2127 3 US-09-764-864-680  
32 72.2 3.3 248 6 US-10-029-386-23112  
33 70.6 3.2 213 6 US-10-029-386-23112  
34 67 3.1 741 9 US-10-779-543-4311  
35 60 2.8 60 3 US-09-908-975-14893  
36 59.2 2.7 597 9 US-10-972-079-90597  
37 52.4 2.4 449 3 US-09-918-995-2523  
38 49.2 2.3 463 3 US-09-918-995-2522  
39 47.4 2.2 65 3 US-09-908-975-29690  
40 47.2 2.2 3399 8 US-10-793-639-600  
41 46 2.1 671 5 US-10-184-644-346  
42 46 2.1 671 5 US-10-184-644-346  
43 46 2.1 382256 9 US-10-820-226-1  
44 46 2.1 382259 10 US-11-029-984-1  
45 45.8 2.1 583 3 US-09-864-761-20772

#### ALIGNMENTS

RESULT 1  
US-10-623-272-56  
; Sequence 56, Application US/10623272  
; Publication No. US20040053313A1  
; GENERAL INFORMATION:  
; APPLICANT: Gozes, Iillana  
; APPLICANT: Brennen, Douglas E.  
; APPLICANT: Bassan, Merav  
; APPLICANT: Zamostiano, Rachel  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by the Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)  
; FILE REFERENCE: 015280-291200US  
; CURRENT APPLICATION NUMBER: US/10/623,272  
; PRIOR FILING DATE: 2003-07-17  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 56  
; LENGTH: 2181  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE: ...  
; NAME/KEY: CDS  
; LOCATION: (1)..(2181)  
; OTHER INFORMATION: H3 human activity dependent neurotrophic factor  
; OTHER INFORMATION: III (ADNF III) clone  
US-10-623-272-56

Query Match 100.0%; Score 2181; DB 7; Length 2181;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCTTTTACCATCACAGCAGTGTGATCGACTCTCAATACCAAGCCTAACTTAAT 60  
DB 1 CGGCTTTTACCATCACAGCAGTGTGATCGACTCTCAATACCAAGCCTAACTTAAT 60  
QY 61 TCTACAGGAGTCAACATGATGTCAGTGTTCATCTGACGACGACAACTATGGAGTCAAA 120  
DB 61 TCTACAGGAGTCAACATGATGTCAGTGTTCATCTGACGACGACAACTATGGAGTCAAA 120

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OM nucleic - nucleic search, using sw model

Run on: March 27, 2006, 18:03:33 ; Search time 365.097 Seconds

(without alignments)  
10618.724 Million cell updates/sec

Title: US-10-623-272-56

Perfect score: 2181

Sequence: 1 CGGCTTACCATCACAGCA.....aaggctaccatgcaaggtga 2181

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /cgn2.6/prodata/1/ina/1 COMB.seq.\*
- 2: /cgn2.6/prodata/1/ina/5 COMB.seq.\*
- 3: /cgn2.6/prodata/1/ina/6A COMB.seq.\*
- 4: /cgn2.6/prodata/1/ina/6B COMB.seq.\*
- 5: /cgn2.6/prodata/1/ina/H COMB.seq.\*
- 6: /cgn2.6/prodata/1/ina/PCITUS COMB.seq.\*
- 7: /cgn2.6/prodata/1/ina/pp COMB.seq.\*
- 8: /cgn2.6/prodata/1/ina/RE COMB.seq.\*
- 9: /cgn2.6/prodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2181	100.0	2181	3	US-09-187-330-56
2	2169	99.4	4386	3	US-09-364-609-7
3	2169	99.4	4663	3	US-09-620-312D-328
4	2165.8	99.3	4193	3	US-09-187-330-58
5	2140	98.1	4874	3	US-09-187-330-2
6	1715.6	78.7	2487	3	US-09-187-330-54
7	1697.8	77.8	2421	3	US-09-187-330-4
8	606	27.8	607	3	US-09-370-838-251
9	606	27.8	607	3	US-09-854-133-251
10	395	18.1	396	3	US-09-854-133-698
11	383.6	17.6	837	3	US-09-187-330-29
12	383.6	17.6	850	3	US-09-187-330-30
13	215.2	9.9	267	3	US-09-896-569-7
14	55.8	2.6	7218	2	US-08-232-463-14
15	47.2	2.2	3399	3	US-09-614-221A-600
16	44.8	2.1	767677	3	US-09-949-016-12147
17	44.8	2.1	767677	3	US-09-949-016-17361
18	44	2.0	1548	3	US-09-248-796A-6167
19	42	1.9	2277	2	US-08-676-967-2
20	42	1.9	2277	2	US-08-676-974-2
21	42	1.9	2277	2	US-09-098-487-2
22	41.2	1.9	601	3	US-09-949-016-198656
23	40.8	1.9	1664976	3	US-08-916-421B-1
24	40.8	1.9	1664976	3	US-09-692-570-1

c	25	40.6	1.9	505	3	US-09-621-976-15639	Sequence 15639, A
	26	40.2	1.8	4170	3	US-09-976-594-589	Sequence 589, App
	27	40.2	1.8	1664976	3	US-08-916-421B-1	Sequence 1, Appli
	28	40.2	1.8	1664976	3	US-09-692-570-1	Sequence 1, Appli
	29	39.8	1.8	737	4	US-09-605-703B-1245	Sequence 1245, Ap
	30	39.8	1.8	1419	4	US-09-605-703B-1243	Sequence 1243, Ap
	31	39.8	1.8	640681	3	US-09-790-988-1	Sequence 1, Appli
	32	39.6	1.8	1116	3	US-09-248-796A-9660	Sequence 9660, Ap
	33	39.6	1.8	1141	3	US-09-806-708B-22	Sequence 22, Appl
	34	39.6	1.8	7571	3	US-09-949-016-4366	Sequence 4366, Ap
	35	39.6	1.8	8146	3	US-09-976-594-725	Sequence 725, App
	36	39.6	1.8	11917	3	US-09-566-921-32	Sequence 32, Appl
	37	39.6	1.8	101300	3	US-09-949-016-16108	Sequence 16108, A
	38	38.6	1.8	601	3	US-09-949-016-184397	Sequence 184397, A
	39	38.6	1.8	580073	3	US-08-545-528D-1	Sequence 1, Appli
	40	38.2	1.8	2672	3	US-09-214-564A-5	Sequence 5, Appli
	41	38.2	1.8	2815	3	US-09-214-564A-1	Sequence 1, Appli
	42	38	1.7	3095	9	5231168-1	Patent No. 5231168
	43	37.8	1.7	2469	3	US-09-328-352-1628	Sequence 1628, Ap
	44	37.8	1.7	31391	3	US-09-949-016-14319	Sequence 14319, A
	45	37.8	1.7	42376	3	US-09-949-016-16276	Sequence 16276, A

#### ALIGNMENTS

RESULT 1  
US-09-187-330-56  
; Sequence 56, Application US/09187330  
; Patent No. 6613740  
; GENERAL INFORMATION:  
; APPLICANT: Gozes, Illana  
; APPLICANT: Brennenman, Douglas E.  
; APPLICANT: Bassan, Merav  
; APPLICANT: Zamoshtiano, Rachel  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by the Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)  
; FILE REFERENCE: 015280-291200US  
; CURRENT APPLICATION NUMBER: US/09/187,330  
; CURRENT FILING DATE: 1998-11-06  
; EARLIER APPLICATION NUMBER: US 60/037,404  
; EARLIER FILING DATE: 1997-02-07  
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485  
; EARLIER FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 56  
; LENGTH: 2181  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2181)  
; OTHER INFORMATION: H3 human activity dependent neurotrophic factor  
; OTHER INFORMATION: III (ADNF III) clone  
US-09-187-330-56

Query Match	100.0%	Score 2181;	DB 3;	Length 2181;
Best Local Similarity	100.0%;	Pred. No. 0;		
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QY	121	TCCTGAGGCCAGGTTACAGATGTTGGTCAGTCAATGAGACTGGTCTAGGTGGCAACGCA	180	

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OM nucleic - nucleic search, using sw model  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: gb\_est2:\*
- 3: gb\_est3:\*
- 4: gb\_hic:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_est7:\*
- 9: gb\_ges1:\*
- 10: gb\_ges2:\*
- 11: gb\_ges3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1762.8	80.8	3309	11	DQ049565	DQ049565 Pan trogl
4	1715.6	78.7	3951	4	BC057666	BC057666 Mus muscu
5	1703.6	78.1	4607	4	BC052455	BC052455 Mus muscu
6	936	42.9	1071	3	BM463769	BM463769 AGENCOURT
7	897.4	41.1	939	3	CR380124	CR380124 CR980124
8	820.8	37.6	1131	3	BM466393	BM466393 AGENCOURT
9	798	36.6	872	6	CD359989	CD359989 AGENCOURT
10	779.2	35.7	784	7	CR388633	CR388633 CR988633
11	772.4	35.4	937	5	BUI158961	BUI158961 AGENCOURT
12	763	35.0	990	8	CV809205	CV809205 AGENCOURT
13	747.2	34.3	2272	4	BC029302	BC029302 Mus muscu
14	738.6	33.9	962	5	BQ963150	BQ963150 AGENCOURT
15	733.2	33.6	794	8	CV756252	CV756252 AGENCOURT
16	714.6	32.8	826	8	DN539719	DN539719 1385527 M
17	703	32.2	915	3	BQ32214	BQ32214 AGENCOURT
18	700.6	32.1	724	1	AW978442	AW978442 EST390551
19	697.6	32.0	875	5	BQ421212	BQ421212 AGENCOURT
20	694	31.8	705	8	CV752173	CV752173 AGENCOURT
21	680	31.2	691	8	CV865793	CV865793 HESCA 6 C
22	678	31.1	817	6	CD657407	CD657407 AGENCOURT

23	677	31.0	864	7	CN646840	ILLUMIGEN
24	671	30.8	697	3	BM148883	BM148883 TCAAP2852
25	670.4	30.7	767	6	CB311734	AGENCOURT
26	670.2	30.7	763	5	BM971641	BM971641 K-EST0213
27	668.4	30.6	681	2	CB155400	K-EST0213
28	665.4	30.5	722	2	BE780345	BE780345 601468445
29	665	30.5	900	5	BQ892917	AGENCOURT
30	658	30.2	862	3	BI660703	603303525
31	656	30.1	726	7	CN310196	170005326
32	654.8	30.0	936	5	BQ887589	AGENCOURT
33	648	29.7	648	6	CB148256	K-EST0204
34	645.2	29.6	1140	2	BE888686	601513082
35	644.4	29.5	690	2	BE897637	601432486
36	642	29.4	744	6	CD110536	AGENCOURT
37	640.6	29.4	727	8	DN422175	LI84216-0
38	635.2	29.1	753	2	BE872269	601446308
39	634.8	29.1	804	8	CK756075	AGENCOURT
40	634.2	29.1	691	8	DN378210	LI838533
41	630.2	28.9	940	2	EG419378	602446062
42	628.8	28.8	797	3	BI684789	603307158
43	624.6	28.6	640	7	CR539590	DKF2p4591
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ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION Homo sapiens ADNP gene, VIRTUAL TRANSCRIPT, partial sequence.  
ACCESSION DQ049564.1 GI:66902763  
VERSION DQ049564.1  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 3309)  
AUTHORS Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Fladel-Alon, A., Tanenbaum, D.M., Civallo, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
TITLE A scan for positively selected genes in the genomes of humans and chimpanzees  
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)  
PUBMED 15969325  
REFERENCE 2 (bases 1 to 3309)  
AUTHORS Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Fladel-Alon, A., Tanenbaum, D.M., Civallo, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
TITLE Direct Submission  
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.  
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ORIGIN  
Query Match 99.4%; Score 2169; DB 11; Length 3309;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2180; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

GenCore version 5.1.7  
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Run-on: March 27, 2006, 17:53:30 ; Search time 10581.6 Seconds  
(without alignments)  
11716.092 Million cell updates/sec

Title: US-10-623-272-56  
Perfect score: 2181  
Sequence: 1 cggctttaccatcacagca.....aaggctaccatgcaaggtga 2181

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: gb\_env.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

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8: gb\_pr.\*

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10: gb\_sts.\*

11: gb\_sy.\*

12: gb\_un.\*

13: gb\_vi.\*

14: gb\_htg.\*

15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2169	99.4	3314	6 CQ727122	Sequence
3	2169	99.4	4386	6 AR430819	Sequence
4	2169	99.4	4386	6 AX081465	Sequence
5	2169	99.4	4462	6 AX274891	Sequence
6	2169	99.4	4663	6 AR338837	Sequence
7	2169	99.4	4682	6 BC090933	Sequence
8	2169	99.4	4713	8 AF250860	Homo sapi
9	2169	99.4	105334	8 HS914P20	Human DNA
10	2165.8	99.3	4193	6 AR392150	Sequence
11	2165.8	99.3	4282	8 AB018327	Homo sapi
12	2165.8	99.3	4942	8 BC075794	Homo sapi
13	2140	98.1	4874	6 BD082199	Sequence
14	2140	98.1	4874	6 AR392137	Sequence
15	1961	89.9	4632	6 AX081469	Sequence
16	1895.2	86.9	166118	4 CT009560	Pig DNA
17	1895.2	86.9	177412	14 CR974565	Sus scrofa
18	1743.2	79.9	172157	14 AC125832	Rattus no

C	19	1743.2	79.9	253693	14	AC093997
	20	1741.6	79.9	2472	9	AF234680
	21	1715.6	78.7	2487	6	AR392148
	22	1715.6	78.7	2487	9	AF068198
	23	1715.6	78.7	4088	9	BC090840
	24	1715.6	78.7	4930	9	AK129214
	25	1715.6	78.7	145263	9	BC005039
	26	1715.6	78.7	186360	14	BC004757
	27	1714	78.6	3846	9	BC050833
	28	1697.8	77.8	2421	6	BD082200
	29	1697.8	77.8	2421	6	AR392138
	30	1553	71.2	1766	6	CQ054429
	31	1553	71.2	1766	6	CQ073670
	32	1553	71.2	1766	6	CQ143266
	33	1553	71.2	1766	6	CQ203099
	34	1553	71.2	1766	6	CQ226457
	35	1553	71.2	1766	6	CQ264598
	36	1553	71.2	1766	6	CQ301688
	37	1553	71.2	1766	6	BD127366
	38	1103.4	50.6	2420	6	BD127366
	39	1103.4	50.6	2420	6	CQ782891
	40	1103.4	50.6	2420	8	AK074926
	41	926.6	42.5	233789	14	AC162696
	42	926.6	42.5	244676	14	AC160170
	43	808.4	37.1	2741	5	CR326295
	44	791.4	36.3	852	6	BD125009
	45	791.4	36.3	852	6	BD127000

## ALIGNMENTS

RESULT 1	AR392149	2181 bp	DNA	linear	PAT 18-DEC-2003
LOCUS	Sequence 56 from patent US 6613740.				
DEFINITION	AR392149				
ACCESSION	AR392149				
VERSION	AR392149.1	GI:40116053			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 2181)				
AUTHORS	Coates, I., Brennan, D.E., Bassan, M. and Zamostiano, R.				
TITLE	Activity dependent neurotrophic factor III (ADNF III)				
JOURNAL	Patent: US 6613740-A 56 02-SEP-2003;				
	Ramot University Authority for Applied Research and Industrial				
	Development Ltd. and The United States of America as represented by				
	the Secretary of the Department of Health and Human Services; Tel				
	Aviv;				
	ILX;				

FEATURES	Location/Qualifiers
source	1..2181
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Best Local Similarity	100.0%; Pred. No. 0;
Matches 2181; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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Db	61 TCTACAGGAGTCAACATGATGTCAGTGTTCATCTCGACGAGAACATATGAGTCAAA 120
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Db	121 TCTGTAGGCCAGGGTTTACAGTGTGTCAGTCAATGAGACTGGGTCTAGGTGGCAACGCA 180

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 27, 2006, 18:29:37 ; Search time 1772.85 Seconds  
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Title: US-10-623-272-58

Perfect score: 4193

Sequence: 1 aaacaggactactcgagca.....gtaaaaaaaaaaaaaa 4193

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9258654 seqs, 1993127192 residues

Total number of hits satisfying chosen parameters: 18517308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA New:\*

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- 2: /SIDSS/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 3	48.6	1.2	990	10	US-10-301-480-568793
C 4	48.6	1.2	990	10	US-10-301-480-1182202
C 5	48.6	1.2	11049	8	US-10-240-708-24
C 6	45	1.1	627	6	US-09-925-065A-758867
C 7	44.8	1.1	119036	8	US-10-995-561-13314
C 8	44.6	1.1	2249	11	US-11-068-859-10
C 9	44.6	1.1	2249	11	US-11-068-859-169
C 10	44.6	1.1	2249	11	US-11-068-859-171
C 11	44.4	1.1	942	9	US-10-301-480-85636
C 12	44.4	1.1	942	10	US-10-301-480-699045
C 13	44.4	1.1	992	10	US-10-301-480-551759
C 14	44.4	1.1	992	10	US-10-301-480-1165168
C 15	44.4	1.1	1452	9	US-10-932-182A-78450
C 16	44.4	1.1	1452	9	US-10-932-182A-78450
C 17	44	1.0	667	6	US-09-925-065A-626778
C 18	43.8	1.0	865	11	US-11-246-980-1

C 19	43.8	1.0	865	11	US-11-246-980-12	Sequence 12, Appl
C 20	43.8	1.0	1330	11	US-11-246-980-26	Sequence 26, Appl
C 21	43.8	1.0	1337	11	US-11-246-980-24	Sequence 24, Appl
C 22	43.6	1.0	6801	8	US-10-240-708-61	Sequence 61, Appl
C 23	43.4	1.0	2412	9	US-10-932-182A-6042	Sequence 6042, Ap
C 24	43.4	1.0	2412	9	US-10-932-182A-6042	Sequence 6042, Ap
C 25	43	1.0	2518	8	US-10-947-249-55	Sequence 55, Appl
C 26	42.8	1.0	560	6	US-09-925-065A-12869	Sequence 12869, A
C 27	42.8	1.0	560	9	US-10-301-480-114106	Sequence 114106
C 28	42.8	1.0	560	10	US-10-301-480-727515	Sequence 727515,
C 29	42.8	1.0	985	10	US-10-301-480-575940	Sequence 575940,
C 30	42.8	1.0	985	10	US-10-301-480-1189349	Sequence 1189349,
C 31	42.6	1.0	1366	11	US-11-146-428-7	Sequence 7, Appl1
C 32	42.4	1.0	602	6	US-09-925-065A-894255	Sequence 894255,
C 33	42.2	1.0	990	10	US-10-301-480-568794	Sequence 568794,
C 34	42.2	1.0	990	10	US-10-301-480-1182203	Sequence 1182203,
C 35	42.2	1.0	1766	6	US-09-925-065A-38310	Sequence 38310, A
C 36	42.2	1.0	1766	6	US-09-925-065A-38311	Sequence 38311, A
C 37	42.2	1.0	1766	6	US-09-925-065A-38312	Sequence 38312, A
C 38	42.2	1.0	1766	6	US-09-925-065A-38313	Sequence 38313, A
C 39	42.2	1.0	1766	9	US-10-301-480-139548	Sequence 139548,
C 40	42.2	1.0	1766	9	US-10-301-480-139549	Sequence 139549,
C 41	42.2	1.0	1766	9	US-10-301-480-139550	Sequence 139550,
C 42	42.2	1.0	1766	9	US-10-301-480-139551	Sequence 139551,
C 43	42.2	1.0	1766	10	US-10-301-480-752957	Sequence 752957,
C 44	42.2	1.0	1766	10	US-10-301-480-752958	Sequence 752958,
C 45	42.2	1.0	1766	10	US-10-301-480-752959	Sequence 752959,

#### ALIGNMENTS

##### RESULT 1

US-10-301-480-612639/c  
; Sequence 612639, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; PRIOR FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 612639  
; LENGTH: 977  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-612639

Query Match	7.5%	Score 316.4;	DB 10;	Length 977;
Best Local Similarity	99.7%	Pred. No. 3.7e-68;		
Matches 317;	Conservative	0;	Mismatches 1;	Indels 0;
Gaps	0;			
Qy	3863	AAACAAAACTGGTATTTCAGATCTGTTTCTGAAATCTTTTAAGCTTAAATACACATGCA	3922	
Db	977	AAACAAAACTGGTATTTCAGATCTGTTTCTGAAATCTTTTAAGCTTAAATACACATGCA	918	
Qy	3923	AGAATTGACCTTCCAGCTACTAATTTTGACACCTTTTAGATCTGTATTAAGTGTGTGT	3982	
Db	917	AGAATTGACCTTCCAGCTACTAATTTTGACACCTTTTAGATCTGTATTAAGTGTGTGT	858	
Qy	3983	GTTGAAGCAGCAACCAATGAGTCTGCTGATTTTGGATTTTATTTATCTTTAGTTCAA	4042	
Db	857	GTTGAAGCAGCAACCAATGAGTCTGCTGATTTTGGATTTTATTTATCTTTAGTTCAA	798	
Qy	4043	CACCATCATGCTGGATTCATTATACCATCTAATATATATGACACACTTCTTACTGTAT	4102	

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OM nucleic - nucleic search, using sw model

Run on: March 27, 2006, 18:11:13 ; Search time 2910.23 Seconds  
(without alignments)  
11914.334 Million cell updates/sec

Title: US-10-623-272-58

Perfect score: 4193

Sequence: 1 aaacaggactatcgga.....gtaaaaaaaaaaaaaa 4193

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:\*

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3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4193	100.0	4193	7	US-10-623-272-58
2	4181.8	99.7	4386	3	Sequence 58, Appl
3	4177.2	99.6	4462	7	Sequence 7, Appl
4	4163.8	99.3	4713	6	Sequence 156, Appl
5	4156.6	99.1	4663	5	Sequence 1, Appl
6	4156.6	99.1	4663	6	Sequence 328, Appl
7	4156.6	99.1	4663	9	Sequence 328, Appl
8	3437.2	82.0	4874	7	Sequence 2, Appl
9	2165.8	51.7	2181	7	Sequence 56, Appl
10	1967.6	46.9	2487	7	Sequence 54, Appl
11	1912.8	45.6	2421	7	Sequence 4, Appl
12	1762.8	42.0	1766	3	Sequence 30357, A
13	671	16.0	673	5	Sequence 137463
14	671	16.0	673	6	Sequence 137463
15	642.2	15.3	702	9	Sequence 7881, Ap
16	606	14.5	607	3	Sequence 251, Ap
17	606	14.5	607	3	Sequence 251, Ap
18	606	14.5	607	5	Sequence 251, Ap
19	593	14.1	741	9	Sequence 4311, Ap
20	593	14.1	741	9	Sequence 4312, Ap
21	547.4	13.1	564	5	Sequence 856, Ap
22	544.2	13.0	549	3	Sequence 17004, A
23	532	12.7	760	9	Sequence 5153, Ap

Sequence 13787, A  
Sequence 179, App  
Sequence 1152, Ap  
Sequence 42054, A  
Sequence 42054, A  
Sequence 28682, A  
Sequence 698, App  
Sequence 698, App  
Sequence 29, Appl  
Sequence 30, Appl  
Sequence 104, App  
Sequence 104, App  
Sequence 1874, Ap  
Sequence 50957, A  
Sequence 50957, A  
Sequence 944, App  
Sequence 942, App  
Sequence 3318, Ap  
Sequence 4017, Ap  
Sequence 3318, Ap  
Sequence 4017, Ap  
Sequence 3318, Ap

11.2 471 3 US-09-864-761-13787  
11.2 470.2 3 US-09-864-761-13787  
10.7 625 3 US-09-969-034-1152  
10.5 463 7 US-10-242-535A-42054  
10.5 463 7 US-10-085-783A-42054  
9.4 453 3 US-09-918-995-28682  
9.4 396 3 US-09-854-133-698  
9.4 396 5 US-10-144-649A-698  
9.1 937 7 US-10-623-272-29  
9.1 850 7 US-10-623-272-30  
8.3 352 3 US-09-777-564-104  
8.3 352 5 US-10-015-219-104  
7.4 399 3 US-09-960-352-1874  
7.2 355 7 US-10-242-535A-50957  
7.2 355 7 US-10-085-783A-50957  
6.8 300 9 US-10-779-543-944  
6.8 300 9 US-10-779-543-942  
6.4 270 3 US-09-796-692-3318  
6.4 270 3 US-09-796-692-4017  
6.4 270 5 US-10-040-862-3318  
6.4 270 5 US-10-040-862-4017  
6.4 270 6 US-10-057-475B-3318

#### ALIGNMENTS

RESULT 1  
US-10-623-272-58  
; Sequence 58, Application US/10623272  
; Publication No. US20040053313A1  
; GENERAL INFORMATION:  
; APPLICANT: Gozes, Ilana  
; APPLICANT: Brennenman, Douglas E.  
; APPLICANT: Bassan, Merav  
; APPLICANT: Zamostiano, Rachel  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by the Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)  
; FILE REFERENCE: 015280-291200US  
; CURRENT APPLICATION NUMBER: US/10/623,272  
; CURRENT FILING DATE: 2003-07-17  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 58  
; LENGTH: 4193  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE: ...  
; NAME/KEY: CDS  
; LOCATION: (492)..(3116)  
; OTHER INFORMATION: H7 human activity dependent neurotrophic factor  
; OTHER INFORMATION: III (ADNF III) clone  
US-10-623-272-58

Query Match 100.0%; Score 4193; DB 7; Length 4193;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAACAGGACTATCGACAAACCTTCTGTCGAGCGCTTGTCCATTTTCTCAAAAT 60  
Db 1 AAACAGGACTATCGACAAACCTTCTGTCGAGCGCTTGTCCATTTTCTCAAAAT 60  
QY 61 TCCTCTCTGCTACAAAAGTCATTTCGCGCAATGTCCATAGTGAAGACTTTGAAATAGGA 120  
Db 61 TCCTCTCTGCTACAAAAGTCATTTCGCGCAATGTCCATAGTGAAGACTTTGAAATAGGA 120



Result No.	Score	Query Match	§			DB	ID	Description
			Length	Length	Length			
1	4193	100.0	4193	3	US-09-187-330-58	Sequence 58, Appl		
2	4181.8	99.7	4386	3	US-09-364-603-7	Sequence 7, Appl		
3	4156.6	99.1	4663	3	US-09-620-312D-328	Sequence 328, App		
4	3437.2	82.0	4874	3	US-09-187-330-2	Sequence 2, Appl		
5	2165.8	51.7	2181	3	US-09-187-330-56	Sequence 56, Appl		
6	1967.6	46.9	2487	3	US-09-187-330-54	Sequence 54, Appl		
7	1912.8	45.6	2421	3	US-09-187-330-4	Sequence 4, Appl		
8	606	14.5	607	3	US-09-370-838-251	Sequence 251, App		
9	606	14.5	607	3	US-09-854-133-251	Sequence 251, App		
10	436.8	10.4	529	3	US-09-306-564-2	Sequence 2, Appl		
11	395	9.4	396	3	US-09-854-133-698	Sequence 698, App		
12	383.6	9.1	837	3	US-09-187-330-29	Sequence 29, Appl		
13	383.6	9.1	850	3	US-09-187-330-30	Sequence 30, Appl		
14	215.2	5.1	267	3	US-09-696-569-7	Sequence 7, Appl		
15	62.4	1.5	7218	2	US-08-232-463-14	Sequence 14, Appl		
16	53.4	1.3	1141	3	US-09-806-708B-22	Sequence 22, Appl		
17	50	1.2	50	3	US-09-187-330-61	Sequence 61, Appl		
18	49.6	1.2	832	3	US-09-621-976-2813	Sequence 2813, Ap		
19	49	1.2	55886	3	US-09-949-016-15129	Sequence 15129, A		
20	48.8	1.2	3399	3	US-09-614-221A-600	Sequence 600, App		
21	48.4	1.2	50	3	US-09-187-330-63	Sequence 63, Appl		
22	48.4	1.2	187169	3	US-09-949-016-12776	Sequence 12776, A		
23	48.4	1.2	191569	3	US-09-949-016-15940	Sequence 15940, A		
24	47.8	1.1	2238	2	US-08-919-624-2	Sequence 2, Appl		

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OM nucleic - nucleic search, using sw model

Run on: March 27, 2006, 17:54:31 ; Search time 15897.7 Seconds  
(without alignments)  
12340.003 Million cell updates/sec

Title: US-10-623-272-58

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Sequence: 1 aaaccggactatcgagca.....gtaaaaaaaaaaaaaa 4193

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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8: gb\_est7:.\*  
9: gb\_gss1:.\*  
10: gb\_gss2:.\*  
11: gb\_gss3:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	4082.2	97.4	4142	4	HSM800682
2	3108	74.1	3309	11	DO049564
3	3079.4	73.4	4607	4	BC052455
4	2854.6	68.1	3951	4	BC057666
5	2237.4	53.4	3309	11	DO049565
6	1663	39.7	1671	4	BC015554
7	1346.4	32.1	2272	4	BC029302
8	994.8	23.7	1576	4	AK079160
9	936	22.3	1071	3	BM463769
10	897.4	21.4	939	7	CR980124
11	820.8	19.6	1131	3	BM466393
12	809	19.3	900	5	BQ892917
13	798	19.0	872	6	CD359989
14	793.6	18.9	864	7	CN646840
15	782.8	18.7	797	8	CX164702
16	782.2	18.7	949	7	CO647981
17	779.2	18.6	784	7	CR988633
18	769.2	18.3	937	5	BUI58961
19	763	18.2	890	8	CV809205
20	760	18.1	782	6	CA418550
21	759.4	18.1	797	3	BM479997
22	758.2	18.1	1145	2	BG028863

23	751.8	17.9	868	8	DN115885
24	751.2	17.9	806	2	BG574926
25	738.6	17.6	962	5	BQ963150
26	730.4	17.4	794	8	CK756252
27	726	17.3	726	7	CN310196
28	718.2	17.1	811	8	DN538297
29	714.6	17.0	826	8	DN539719
30	713.4	17.0	715	3	BM786807
31	713	17.0	755	6	CA313085
32	711.8	17.0	739	5	BQ622230
33	709.8	16.9	774	5	BUT732902
34	704.8	16.8	716	6	CB306753
35	703	16.8	915	3	BQ232214
36	701.4	16.7	875	5	BQ421212
37	701	16.7	722	3	BM678487
38	700.6	16.7	724	1	AW978442
39	700	16.7	820	2	BG615791
40	698.8	16.7	760	8	CK763245
41	698.2	16.7	801	2	BBS35959
42	697.4	16.6	883	8	DN116241
43	694	16.6	705	8	CK752173
44	692.6	16.5	784	7	CO737136
45	691.6	16.5	847	7	CV557837

#### ALIGNMENTS

RESULT 1  
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LOCUS Homo sapiens mRNA; cDNA DKFZp586K2120 (from clone DKFZp586K2120).  
DEFINITION  
ACCESSION AL080163  
VERSION AL080163.1 GI:5262626  
KEYWORDS HTC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 4142)  
Wambutt, R., Heubner, D., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.  
AUTHORS The German cDNA Consortium  
COMMENT Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY  
Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Agowa (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.  
This clone (DKFZp586K2120) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:  
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp586K2120  
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.  
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Location/Qualifiers  
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/mol\_type="mRNA"  
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/clone="DKFZp586K2120"  
/tissue\_type="uterus"  
/clone\_lib="586 (synonym: hutel). Vector pSport1; host DH10B; Sites NotI + SalI/MluI"  
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1. 4142  
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OM nucleic - nucleic search, using sw model

Run on: March 27, 2006, 17:41:56 ; Search time 2197.81 Seconds  
(without alignments)  
12714.981 Million cell updates/sec

Title: US-10-623-272-58  
Perfect score: 4193  
Sequence: 1 aaaccaggactatcgac.....gtaaaaaaaaaaaaaa 4193

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
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3: geneseqn2000s.\*  
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5: geneseqn2001bs.\*  
6: geneseqn2002as.\*  
7: geneseqn2002bs.\*  
8: geneseqn2003as.\*  
9: geneseqn2003bs.\*  
10: geneseqn2003cs.\*  
11: geneseqn2003ds.\*  
12: geneseqn2004as.\*  
13: geneseqn2004bs.\*  
14: geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4193	100.0	4193	3	Aad00750 Human Act
2	4181.8	99.7	4386	4	Aaf54895 Human act
3	4177.2	99.6	4462	5	Abas3022 Human tra
4	4163.8	99.3	4713	9	Ada07950 Human act
5	4162.2	99.3	4713	14	Adx06276 Cyclin-de
6	4156.6	99.1	4663	4	Aai58447 Human pol
7	4156.6	99.1	4663	5	Adq98658 DNA encod
8	4156.6	99.1	4663	9	Adb48418 Novel hum
9	4120.2	98.3	4554	4	Aai60233 Human pol
10	3973.8	94.8	4632	4	Aaf54902 Human act
11	3437.2	82.0	4874	2	Aav49807 Human ADN
12	3437.2	82.0	4874	3	Aad00746 Human Act
13	2397.8	57.2	2420	4	Aak94337 Human ful
14	2397.8	57.2	2420	12	Adl30998 Full leng
15	2165.8	51.7	2181	3	Aad00749 Human act
16	1967.6	46.9	2487	3	Aad00748 Mouse Act
17	1912.8	45.6	2421	2	Aav49808 Mouse ADN
18	1912.8	45.6	2421	3	Aad00747 Mouse Act
19	1762.8	42.0	1766	4	Aai19537 Probe #94

C	20	1762.8	42.0	1766	4	ABA64554	Abas64554 Human foe
C	21	1762.8	42.0	1766	4	AAI44727	Aai44727 Probe #13
C	22	1762.8	42.0	1766	4	ABA46681	Abas46681 Human bre
C	23	1762.8	42.0	1766	4	AAK38731	Aak38731 Human bon
C	24	1762.8	42.0	1766	4	ABS38306	Abas38306 Human liv
C	25	1762.8	42.0	1766	5	AAI05258	Aai05258 Probe #52
C	26	1762.8	42.0	1766	5	ABSI2802	Abas12802 Human gen
C	27	789.8	18.8	852	4	AAK91980	Aak91980 Human CDN
C	28	789.8	18.8	852	4	AAK93971	Aak93971 Human CDN
C	29	789.8	18.8	852	12	ADL30398	Adl30398 5' end of
C	30	789.8	18.8	852	12	ADL28407	Adl28407 5' end of
C	31	721.4	17.2	880	2	AAK39927	Aak39927 Gastric c
C	32	720.8	17.2	838	2	AAK39926	Aak39926 Gastric c
C	33	689.2	16.4	772	4	AAK93336	Aak93336 Human CDN
C	34	689.2	16.4	772	12	ADL29763	Adl29763 5' end of
C	35	642.2	15.3	702	3	AAA01794	Aaa01794 Human col
C	36	606	14.5	607	3	AAK79209	Aak79209 Human lun
C	37	606	14.5	607	4	AAK23285	Aak23285 Human lun
C	38	606	14.5	607	10	ADD65559	Ad665559 Human lun
C	39	606	14.5	607	10	ADL87813	Ad87813 Human lun
C	40	605.2	14.4	623	14	ACL55151	Ac155151 Human col
C	41	593	14.1	741	2	AAZ15998	Aaz15998 Human gen
C	42	593	14.1	741	2	AAZ15999	Aaz15999 Human gen
C	43	557.2	13.3	586	4	AAK94032	Aak94032 Human CDN
C	44	557.2	13.3	586	12	ADL30459	Adl30459 3' end of
C	45	547.4	13.1	564	6	ABV95448	Abv95448 Human pan

## ALIGNMENTS

RESULT 1  
AAD00750

ID AAD00750 standard; cDNA; 4193 BP.

AC AAD00750;

XX 08-SEP-2000 (first entry)

XX Human Activity Dependent Neurotrophic Factor (ADNF) III H7 cDNA.

XX Activity Dependent Neurotrophic Factor III; ADNF; human; ADNF;  
XX Activity Dependent Neurotrophic Factor III; ADNF; human; ADNF;  
KW autosomal dominant nocturnal frontal-lobe epilepsy; neuronal cell death;  
KW neurological deficiency; treatment; HIV; Human Immunodeficiency Virus;  
KW Alzheimer's disease; beta-amyloid peptide; Huntington's disease;  
KW epilepsy; AIDS dementia complex; neuropathic pain syndrome; ALS;  
KW amytrophic lateral sclerosis; Parkinson's disease; Leber's disease;  
KW mitochondrial abnormality; Wernicke's encephalopathy; homocysteinuria;  
KW hyperproliferemia; sulphite oxide disease; Tourette's syndrome; nontropic;  
KW Down's syndrome; drug addiction; developmental retardation; antileptic;  
KW learning impairment; anticonvulsant; neuroprotective; anti-HIV; ss.

XX Homo sapiens.

XX Key ... Location/Qualifiers  
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/note= "Activity Dependent Neurotrophic Factor III"

WO200027875-A2.

XX 18-MAY-2000.

XX 04-NOV-1999; 99WO-US026213.

XX 06-NOV-1998; 98US-00187330.

XX (USAS ) GOVERNMENT US REPRESENT AS.  
XX (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

XX Cozes I, Breneman DE, Bassan M, Zamostiano R;

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 27, 2006, 17:53:30 ; Search time 20343.4 Seconds

(without alignments)  
11716.092 Million cell updates/sec

Title: US-10-623-272-58

Perfect score: 4193

Sequence: 1 aaacaggactatcgagca.....gtataaaaaaaaaaaaaa 4193

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.in.\*

3: gb.env.\*

4: gb.on.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pr.\*

9: gb.ro.\*

10: gb.sts.\*

11: gb.sy.\*

12: gb.un.\*

13: gb.vi.\*

14: gb.htg.\*

15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	4193	100.0	4193	6	AR392150 Sequence
2	4181.8	99.7	4386	6	AR430819 Sequence
3	4181.8	99.7	4386	6	AX081465 Sequence
4	4177.2	99.6	4462	6	AX274891 Sequence
5	4174.4	99.6	4682	8	BC090933 Homo sapi
6	4163.8	99.3	4713	8	AF250860 Homo sapi
7	4159	99.2	4282	8	AB018327 Homo sapi
8	4158	99.2	105334	8	HS914P20 Human DNA
9	4156.6	99.1	4663	6	AR338837 Sequence
10	4150.6	99.0	4942	8	BC075794 Homo sapi
11	3973.8	94.8	4632	6	AX081469 Sequence
12	3544.2	84.5	166118	4	CR009560 Pig DNA s
13	3544.2	84.5	177412	14	CR974565
14	3437.2	82.0	4874	6	BD082199 Activity
15	3437.2	82.0	4874	6	AR392137 Sequence
16	3108	74.1	3314	6	CQ727122 Sequence
17	3082.4	73.8	172157	14	AC158832 Rattus no
18	3092.4	73.8	253693	14	AC091997 Rattus no

19	3084.4	73.6	4930	9	AK129214	AK129214 Mus muscu
20	3083.4	73.5	145263	9	EX005039	EX005039 Mouse DNA
21	3083.4	73.5	186960	14	EX004757	EX004757 Mus muscu
22	2978.8	71.0	4088	9	BC090840	BC090840 Mus muscu
23	2767.2	66.0	3846	9	BC050833	BC050833 Mus muscu
24	2397.8	57.2	2420	6	BD127366	BD127366 Primer fo
25	2397.8	57.2	2420	6	CQ782891	CQ782891 Sequence
26	2397.8	57.2	2420	8	AK074826	AK074826 Homo sapi
27	2181	52.0	233789	14	AC162696	AC162696 Bos tauru
28	2181	52.0	244676	14	AC160170	AC160170 Bos tauru
29	2165.8	51.7	2181	6	AR392149	AR392149 Sequence
30	1996.8	47.6	2472	9	AF234680	AF234680 Rattus no
31	1969.2	47.0	2487	9	AF068198	AF068198 Mus muscu
32	1967.6	46.9	2487	6	AR392148	AR392148 Sequence
33	1912.8	45.6	2421	6	BD082200	BD082200 Activity
34	1912.8	45.6	2421	6	AR392138	AR392138 Sequence
35	1762.8	42.0	1766	6	CQ054429	CQ054429 Sequence
36	1762.8	42.0	1766	6	CQ073670	CQ073670 Sequence
37	1762.8	42.0	1766	6	CQ104554	CQ104554 Sequence
38	1762.8	42.0	1766	6	CQ143266	CQ143266 Sequence
39	1762.8	42.0	1766	6	CQ203099	CQ203099 Sequence
40	1762.8	42.0	1766	6	CQ226457	CQ226457 Sequence
41	1762.8	42.0	1766	6	CQ264598	CQ264598 Sequence
42	1762.8	42.0	1766	6	CQ301688	CQ301688 Sequence
43	1260.4	30.1	2741	5	CR926295	CR926295 Xenopus t
44	1003.2	23.9	2730	9	BC066203	BC066203 Mus muscu
45	789.8	18.8	852	6	BD125009	BD125009 Primer fo

#### ALIGNMENTS

RESULT 1	AR392150	AR392150	4193 bp	DNA	linear	PAT 18-DEC-2003
LOCUS	Sequence 58 from patent US 6613740.					
DEFINITION	AR392150					
ACCESSION	AR392150					
VERSION	AR392150.1	GI:40116054				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 4193)					
AUTHORS	Gozes, I., Breneman, D.E., Bassan, M. and Zamostiano, R.					
TITLE	Activity dependent neurotrophic factor III (ADNF III)					
JOURNAL	Patent: US 6613740-A 58 02-SEP-2003;					
	Ramot University Authority for Applied Research and Industrial					
	Development Ltd. and The United States of America as represented by					
	the Secretary of the Department of Health and Human Services; Tel					
	Aviv;					
	ILX;					

FEATURES	Location/Qualifiers
source	1..4193
	/organism="unknown"
	/mol_type="genomic DNA"

ORIGIN	100.0%; Score 4193; DB 6; Length 4193;
Query Match	100.0%; Pred. No. 0;
Best Local Similarity	0; Mismatches 0; Indels 0; Gaps 0;
Matches 4193; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 AAAACACGAGGACTATCGAGCAAAAACCTTTCTGCTGCAGCGCTTGTCCTCAAAAT 60
Db	1 AAAACACGAGGACTATCGAGCAAAAACCTTTCTGCTGCAGCGCTTGTCCTCAAAAT 60
Qy	61 TCTTCTTCTGCTATCGAGCAAAAACCTTTCTGCTGCAGCGCTTGTCCTCAAAATAGGA 120
Db	61 TCTTCTTCTGCTATCGAGCAAAAACCTTTCTGCTGCAGCGCTTGTCCTCAAAATAGGA 120
Qy	121 TTCTCTTCTTCTGCTATCGAGCAAAAACCTTTCTGCTGCAGCGCTTGTCCTCAAAATAGGA 180
Db	121 TTCTCTTCTTCTGCTATCGAGCAAAAACCTTTCTGCTGCAGCGCTTGTCCTCAAAATAGGA 180